

SEQUENCE LISTING

<110> NIPPON MEDICAL SCHOOL FOUNDATION

<120> Cell death-inducing fusion gene specifically acting on cancer and
gene product thereof

<130> PH-2011-PCT

<140>

<141>

<150> JP2003/081337

<151> 2003-03-24

<160> 27

<170> PatentIn Ver. 2.1

<210> 1

<211> 579

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1).. (579)

<400> 1

atg gac ggg tcc ggg gag cag ccc aga ggc ggg ggg ccc acc agc tct 48

Met Asp Gly Ser Gly Glu Gln Pro Arg Gly Gly Gly Pro Thr Ser Ser

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gag cag atc atg aag aca ggg gcc ctt ttg ctt cag ggt ttc atc cag				96
Glu Gln Ile Met Lys Thr Gly Ala Leu Leu Leu Gln Gly Phe Ile Gln				
20	25	30		
gat cga gca ggg cga atg ggg ggg gag gca ccc gag ctg gcc ctg gac				144
Asp Arg Ala Gly Arg Met Gly Gly Glu Ala Pro Glu Leu Ala Leu Asp				
35	40	45		
ccg gtg cct cag gat gcg tcc acc aag aag ctg agc gag tgt ctc aag				192
Pro Val Pro Gln Asp Ala Ser Thr Lys Lys Leu Ser Glu Cys Leu Lys				
50	55	60		
cgc atc ggg gac gaa ctg gac agt aac atg gag ctg cag agg atg att				240
Arg Ile Gly Asp Glu Leu Asp Ser Asn Met Glu Leu Gln Arg Met Ile				
65	70	75	80	
gcc gcc gtg gac aca gac tcc ccc cga gag gtc ttt ttc cga gtg gca				288
Ala Ala Val Asp Thr Asp Ser Pro Arg Glu Val Phe Phe Arg Val Ala				
85	90	95		
gct gac atg ttt tct gac ggc aac ttc aac tgg ggc cgg gtt gtc gcc				336
Ala Asp Met Phe Ser Asp Gly Asn Phe Asn Trp Gly Arg Val Val Ala				
100	105	110		
ctt ttc tac ttt gcc agc aaa ctg gtg ctc aag gcc ctg tgc acc aag				384
Leu Phe Tyr Phe Ala Ser Lys Leu Val Leu Lys Ala Leu Cys Thr Lys				
115	120	125		

gtg ccg gaa ctg atc aga acc atc atg ggc tgg aca ttg gac ttc ctc 432
 Val Pro Glu Leu Ile Arg Thr Ile Met Gly Trp Thr Leu Asp Phe Leu
 130 135 140

cgg gag cgg ctg ttg ggc tgg atc caa gac cag ggt ggt tgg gac ggc 480
 Arg Glu Arg Leu Leu Gly Trp Ile Gln Asp Gln Gly Gly Trp Asp Gly
 145 150 155 160

ctc ctc tcc tac ttt ggg acg ccc acg tgg cag acc gtg acc atc ttt 528
 Leu Leu Ser Tyr Phe Gly Thr Pro Thr Trp Gln Thr Val Thr Ile Phe
 165 170 175

gtg gcg gga gtg ctc acc gcc tcg ctc acc atc tgg aag aag atg ggc 576
 Val Ala Gly Val Leu Thr Ala Ser Leu Thr Ile Trp Lys Lys Met Gly
 180 185 190

tga 579

<210> 2

<211> 192

<212> PRT

<213> Homo sapiens

<400> 2

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 Glu Gln Ile Met Lys Thr Gly Ala Leu Leu Leu Gln Gly Phe Ile Gln
 20 25 30
 Asp Arg Ala Gly Arg Met Gly Gly Glu Ala Pro Glu Leu Ala Leu Asp

35	40	45
Pro Val Pro Gln Asp Ala Ser Thr Lys Lys Leu Ser Glu Cys Leu Lys		
50	55	60
Arg Ile Gly Asp Glu Leu Asp Ser Asn Met Glu Leu Gln Arg Met Ile		
65	70	75
Ala Ala Val Asp Thr Asp Ser Pro Arg Glu Val Phe Phe Arg Val Ala		
85	90	95
Ala Asp Met Phe Ser Asp Gly Asn Phe Asn Trp Gly Arg Val Val Ala		
100	105	110
Leu Phe Tyr Phe Ala Ser Lys Leu Val Leu Lys Ala Leu Cys Thr Lys		
115	120	125
Val Pro Glu Leu Ile Arg Thr Ile Met Gly Trp Thr Leu Asp Phe Leu		
130	135	140
Arg Glu Arg Leu Leu Gly Trp Ile Gln Asp Gln Gly Gly Trp Asp Gly		
145	150	155
Leu Leu Ser Tyr Phe Gly Thr Pro Thr Trp Gln Thr Val Thr Ile Phe		
165	170	175
Val Ala Gly Val Leu Thr Ala Ser Leu Thr Ile Trp Lys Lys Met Gly		
180	185	190

<210> 3

<211> 999

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1).. (999)

<400> 3

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ggc gag gaa ctg ttc act ggc gtg gtc cca att ctc gtg gaa ctg gat 96
Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val Glu Leu Asp
20 25 30

ggc gat gtg aat ggg cac aaa ttt tct gtc agc gga gag ggt gaa ggt 144
Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu Gly Glu Gly
35 40 45

gat gcc aca tac gga aag ctc acc ctg aaa ttc atc tgc acc act gga 192
Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly
50 55 60

aag ctc cct gtg cca tgg cca aca ctg gtc act acc ttc acc tat ggc 240
Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe Thr Tyr Gly
65 70 75 80

gtg cag tgc ttt tcc aga tac cca gac cat atg aag cag cat gac ttt 288
Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln His Asp Phe
85 90 95

ttc aag agc gcc atg ccc gag ggc tat gtg cag gag aga acc atc ttt 336
Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe
100 105 110

ttc aaa gat gac ggg aac tac aag acc cgc gct gaa gtc aag ttc gaa 384
Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu
115 120 125

ggt gac acc ctg gtg aat aga atc gag ctg aag ggc att gac ttt aag 432
Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys
130 135 140

gag gat gga aac att ctc ggc cac aag ctg gaa tac aac tat aac tcc 480
Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser
145 150 155 160

cac aat gtg tac atc atg gcc gac aag caa aag aat ggc atc aag gtc 528
His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val
165 170 175

aac ttc aag atc aga cac aac att gag gat gga tcc gtg cag ctg gcc 576
Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala
180 185 190

gac cat tat caa cag aac act cca atc ggc gac ggc cct gtg ctc ctc 624
Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu
195 200 205

cca gac aac cat tac ctg tcc acc cag tct gcc ctg tct aaa gat ccc 672
Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro
210 215 220

aac gaa aag aga gac cac atg gtc ctg ctg gag ttt gtg acc gct gct 720
Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala

225	230	235	240	
ggg atc aca cat ggc atg gac gag ctg tac aag gcc ctt ttc tac ttt				768
Gly Ile Thr His Gly Met Asp Glu Leu Tyr Lys Ala Leu Phe Tyr Phe				
	245	250	255	
gcc agc aaa ctg gtg ctc aag gcc ctg tgc acc aag gtg ccg gaa ctg				816
Ala Ser Lys Leu Val Leu Lys Ala Leu Cys Thr Lys Val Pro Glu Leu				
	260	265	270	
atc aga acc atc atg ggc tgg aca ttg gac ttc ctc cgg gag cgg ctg				864
Ile Arg Thr Ile Met Gly Trp Thr Leu Asp Phe Leu Arg Glu Arg Leu				
	275	280	285	
ttg ggc tgg atc caa gac cag ggt ggt tgg gac ggc ctc ctc tcc tac				912
Leu Gly Trp Ile Gln Asp Gln Gly Gly Trp Asp Gly Leu Leu Ser Tyr				
	290	295	300	
ttt ggg acg ccc acg tgg cag acc gtg acc atc ttt gtg gcg gga gtg				960
Phe Gly Thr Pro Thr Trp Gln Thr Val Thr Ile Phe Val Ala Gly Val				
305	310	315	320	
ctc acc gcc tca ctc acc atc tgg aag aag atg ggc tga				999
Leu Thr Ala Ser Leu Thr Ile Trp Lys Lys Met Gly				
	325	330		

<210> 4

<211> 332

<212> PRT

<213> Homo sapiens

<400> 4

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			20					25					30		
Gly	Asp	Val	Asn	Gly	His	Lys	Phe	Ser	Val	Ser	Gly	Glu	Gly	Glu	Gly
		35				40					45				
Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Phe	Ile	Cys	Thr	Thr	Gly
	50					55				60					
Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr	Phe	Thr	Tyr	Gly
65					70					75				80	
Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro	Asp	His	Met	Lys	Gln	His	Asp	Phe
				85					90				95		
Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu	Arg	Thr	Ile	Phe
			100					105					110		
Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu	Val	Lys	Phe	Glu
		115					120					125			
Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly	Ile	Asp	Phe	Lys
		130				135					140				
Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr	Asn	Tyr	Asn	Ser
145				150					155				160		
His	Asn	Val	Tyr	Ile	Met	Ala	Asp	Lys	Gln	Lys	Asn	Gly	Ile	Lys	Val
				165					170				175		
Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	Glu	Asp	Gly	Ser	Val	Gln	Leu	Ala
		180					185					190			
Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	Ile	Gly	Asp	Gly	Pro	Val	Leu	Leu
		195					200					205			
Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr	Gln	Ser	Ala	Leu	Ser	Lys	Asp	Pro
	210					215						220			

Asn	Glu	Lys	Arg	Asp	His	Met	Val	Leu	Leu	Glu	Phe	Val	Thr	Ala	Ala
225						230				235					240
Gly	Ile	Thr	His	Gly	Met	Asp	Glu	Leu	Tyr	Lys	Ala	Leu	Phe	Tyr	Phe
				245					250					255	
Ala	Ser	Lys	Leu	Val	Leu	Lys	Ala	Leu	Cys	Thr	Lys	Val	Pro	Glu	Leu
			260					265					270		
Ile	Arg	Thr	Ile	Met	Gly	Trp	Thr	Leu	Asp	Phe	Leu	Arg	Glu	Arg	Leu
		275					280					285			
Leu	Gly	Trp	Ile	Gln	Asp	Gln	Gly	Gly	Trp	Asp	Gly	Leu	Leu	Ser	Tyr
	290					295					300				
Phe	Gly	Thr	Pro	Thr	Trp	Gln	Thr	Val	Thr	Ile	Phe	Val	Ala	Gly	Val
305					310					315				320	
Leu	Thr	Ala	Ser	Leu	Thr	Ile	Trp	Lys	Lys	Met	Gly				
				325						330					

<210> 5

<211> 987

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(987)

<400> 5

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15

ttc act ggc gtg gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat	96
Phe Thr Gly Val Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn	
20 25 30	
ggg cac aaa ttt tct gtc agc gga gag ggt gaa ggt gat gcc aca tac	144
Gly His Lys Phe Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr	
35 40 45	
gga aag ctc acc ctg aaa ttc atc tgc acc act gga aag ctc cct gtg	192
Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val	
50 55 60	
cca tgg cca aca ctg gtc act acc ttc acc tat ggc gtg cag tgc ttt	240
Pro Trp Pro Thr Leu Val Thr Thr Phe Thr Tyr Gly Val Gln Cys Phe	
65 70 75 80	
tcc aga tac cca gac cat atg aag cag cat gac ttt ttc aag agc gcc	288
Ser Arg Tyr Pro Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala	
85 90 95	
atg ccc gag ggc tat gtg cag gag aga acc atc ttt ttc aaa gat gac	336
Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp	
100 105 110	
ggg aac tac aag acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg	384
Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu	
115 120 125	
gtg aat aga atc gag ctg aag ggc att gac ttt aag gag gat gga aac	432
Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn	

130	135	140	
att ctc ggc cac aag ctg gaa tac aac tat aac tcc cac aat gtg tac			480
Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr			
145	150	155	160
atc atg gcc gac aag caa aag aat ggc atc aag gtc aac ttc aag atc			528
Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile			
	165	170	175
aga cac aac att gag gat gga tcc gtg cag ctg gcc gac cat tat caa			576
Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln			
	180	185	190
cag aac act cca atc ggc gac ggc cct gtg ctc ctc cca gac aac cat			624
Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His			
	195	200	205
tac ctg tcc acc cag tct gcc ctg tct aaa gat ccc aac gaa aag aga			672
Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg			
	210	215	220
gac cac atg gtc ctg ctg gag ttt gtg acc gct gct ggg atc aca cat			720
Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His			
225	230	235	240
ggc atg gac gag ctg tac aag gcc ctt ttc tac ttt gcc agc aaa ctg			768
Gly Met Asp Glu Leu Tyr Lys Ala Leu Phe Tyr Phe Ala Ser Lys Leu			
	245	250	255

gtg ctc aag gcc ctg tgc acc aag gtg ccg gaa ctg atc aga acc atc 816
 Val Leu Lys Ala Leu Cys Thr Lys Val Pro Glu Leu Ile Arg Thr Ile
 260 265 270

atg ggc tgg aca ttg gac ttc ctc cgg gag cgg ctg ttg ggc tgg atc 864
 Met Gly Trp Thr Leu Asp Phe Leu Arg Glu Arg Leu Leu Gly Trp Ile
 275 280 285

caa gac cag ggt ggt tgg gac ggc ctc ctc tcc tac ttt ggg acg ccc 912
 Gln Asp Gln Gly Gly Trp Asp Gly Leu Leu Ser Tyr Phe Gly Thr Pro
 290 295 300

acg tgg cag acc gtg acc atc ttt gtg gcg gga gtg ctc acc gcc tca 960
 Thr Trp Gln Thr Val Thr Ile Phe Val Ala Gly Val Leu Thr Ala Ser
 305 310 315 320

ctc acc atc tgg aag aag atg ggc tga 987
 Leu Thr Ile Trp Lys Lys Met Gly
 325

<210> 6

<211> 328

<212> PRT

<213> Homo sapiens

<400> 6

Met Ala Cys Asn Gly Arg Cys Gly Gly Met Ser Lys Gly Glu Glu Leu
 1 5 10 15
 Phe Thr Gly Val Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn

	20	25	30
Gly His Lys Phe Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr			
35	40	45	
Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val			
50	55	60	
Pro Trp Pro Thr Leu Val Thr Thr Phe Thr Tyr Gly Val Gln Cys Phe			
65	70	75	80
Ser Arg Tyr Pro Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala			
85	90	95	
Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp			
100	105	110	
Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu			
115	120	125	
Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn			
130	135	140	
Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr			
145	150	155	160
Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile			
165	170	175	
Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln			
180	185	190	
Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His			
195	200	205	
Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg			
210	215	220	
Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His			
225	230	235	240
Gly Met Asp Glu Leu Tyr Lys Ala Leu Phe Tyr Phe Ala Ser Lys Leu			
245	250	255	
Val Leu Lys Ala Leu Cys Thr Lys Val Pro Glu Leu Ile Arg Thr Ile			

260	265	270
Met Gly Trp Thr Leu Asp Phe Leu Arg Glu Arg Leu Leu Gly Trp Ile		
275	280	285
Gln Asp Gln Gly Gly Trp Asp Gly Leu Leu Ser Tyr Phe Gly Thr Pro		
290	295	300
Thr Trp Gln Thr Val Thr Ile Phe Val Ala Gly Val Leu Thr Ala Ser		
305	310	315
Leu Thr Ile Trp Lys Lys Met Gly		320
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<210> 7

<211> 9

<212> PRT

<213> Artificial Sequence

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<223> Description of Artificial Sequence:Homing peptide

<400> 7

Cys Leu Ser Ser Arg Leu Asp Ala Cys

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<210> 8

<211> 9

<212> PRT

<213> Artificial Sequence

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<223> Description of Artificial Sequence:Homing peptide

<400> 8

Cys Asn Ser Arg Leu His Leu Arg Cys

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<210> 9

<211> 9

<212> PRT

<213> Artificial Sequence

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<223> Description of Artificial Sequence:Homing peptide

<400> 9

Cys Glu Asn Trp Trp Gly Asp Val Cys

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<210> 10

<211> 21

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Homing peptide

<400> 10

Trp Arg Cys Val Leu Arg Glu Gly Pro Ala Gly Gly Cys Ala Trp Phe

1

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10

15

Asn Arg His Arg Leu

20

<210> 11

<211> 7

<212> PRT

<213> Artificial Sequence

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<223> Description of Artificial Sequence:Homing peptide

<400> 11

Cys Leu Pro Val Ala Ser Cys

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<210> 12

<211> 7

<212> PRT

<213> Artificial Sequence

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<223> Description of Artificial Sequence:Homing peptide

<400> 12

Cys Gly Ala Arg Glu Met Cys

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<210> 13

<211> 9

<212> PRT

<213> Artificial Sequence

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<223> Description of Artificial Sequence:Homing peptide

<400> 13

Cys Lys Ser Thr His Asp Arg Leu Cys

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<210> 14

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Homing peptide

<400> 14

Cys Gly Asn Lys Arg Thr Arg Gly Cys

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<210> 15

<211> 5

<212> .PRT

<213> Artificial Sequence

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<223> Description of Artificial Sequence:Homing peptide

<400> 15

Ala Pro Arg Pro Gly

1 5

<210> 16

<211> 6

<212> PRT

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<223> Description of Artificial Sequence:Homing peptide

<400> 16

Lys Gln Ala Gly Asp Val

1 5

<210> 17

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Homing peptide

<400> 17

Lys Arg Leu Asp Gly Ser

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<210> 18

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Homing peptide

<400> 18

Asp Gly Glu Ala

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<210> 19

<211> 28

<212> DNA

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<223> Description of Artificial Sequence:Primer

<220>

<221> misc_feature

<222> (1).. (2)

<223> n is A, C, G or T

<400> 19

nnatcgatcc accatgagca agggcgag

28

<210> 20

<211> 35

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Primer

<400> 20

ctggcaaagt agaaaagggc cttgtacagc tcgtc

35

<210> 21

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Primer

<400> 21

gcccttttct actttgccag

20

<210> 22

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Primer

<220>

<221> misc_feature

<222> (1).. (2)

<223> n is A, C, G or T

<400> 22

nntctagatc agcccatctt cttcca

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<210> 23

<211> 57

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Primer

<400> 23

ccatggcctg cgattgccgt ggtgattgtt tttgtggtgg tatgagcaag ggcgagg

57

<210> 24

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Primer

<220>

<221> misc_feature

<222> (1)..(4)

<223> n is A, C, G or T

<400> 24

nnnnccatgg cctgcgattg cc

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<210> 25

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Primer

<400> 25

tggaagca ctgcacgc

18

<210> 26

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Primer

<400> 26

ccatggcctg caacggctgt tgcggtggta tgagcaaggg cgagg

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<210> 27

<211> 22

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence:Primer

<220>

<221> misc_feature

<222> (1)..(4)

<223> n is A, C, G or T

<400> 27

nnnnccatgg cctgcaacgg tc

22